RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/581,757_

Source: _____ _1 fwP_

Date Processed by STIC: _____ _6/14/06_

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IFWP

RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: US/10/581,757   TIME: 10:45:02

Input Set : **E:\SEQLIST.TXT**
Output Set: **N:\CRF4\06142006\J581757.raw**

```
   3 <110> APPLICANT: YAMASAKI, SHINJI
   4         ASAKURA, MASAHIRO
   6 <120> TITLE OF INVENTION: CYTOLETHAL DISTENDING TOXINS AND DETECTION OF
   7        CAMPYLOBACTER BACTERIA USING THE SAME AS A TARGET
   9 <130> FILE REFERENCE: SHIM-018
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/581,757
C--> 11 <141> CURRENT FILING DATE: 2006-06-05
  11 <150> PRIOR APPLICATION NUMBER: JP 2003-408103
  12 <151> PRIOR FILING DATE: 2003-12-05
  14 <160> NUMBER OF SEQ ID NOS: 79
  16 <170> SOFTWARE: PatentIn version 3.1
  18 <210> SEQ ID NO: 1
  19 <211> LENGTH: 2211
  20 <212> TYPE: DNA
  21 <213> ORGANISM: Campylobacter coli
  23 <220> FEATURE:
  24 <221> NAME/KEY: CDS
  25 <222> LOCATION: (1)..(777)
  27 <220> FEATURE:
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  29 <222> LOCATION: (802)..(1605)
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  33 <222> LOCATION: (1615)..(2187)
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  39 1               5                   10                  15
  41 ttt tta gct tgt tct tca aaa gaa caa caa atc aat cct tta gga aga      96
  42 Phe Leu Ala Cys Ser Ser Lys Glu Gln Gln Ile Asn Pro Leu Gly Arg
  43             20                  25                  30
  45 tct tac ggt aaa ttt aac gat aac gat cct tta aaa ctt ggt tca aaa     144
  46 Ser Tyr Gly Lys Phe Asn Asp Asn Asp Pro Leu Lys Leu Gly Ser Lys
  47         35                  40                  45
  49 cct aca ccc cct gtc aaa caa aaa aca cca agc ttg gta gaa ggt aaa     192
  50 Pro Thr Pro Pro Val Lys Gln Lys Thr Pro Ser Leu Val Glu Gly Lys
  51     50                  55                  60
  53 aaa ttt ccc gcc ata cca ctt gtc cca cct gta atc act cct aat acc     240
  54 Lys Phe Pro Ala Ile Pro Leu Val Pro Pro Val Ile Thr Pro Asn Thr
  55 65                  70                  75                  80
  57 ttt aaa gga gat aat gcc gtc aaa ggc cca ttg cca agg cta aaa tct     288
  58 Phe Lys Gly Asp Asn Ala Val Lys Gly Pro Leu Pro Arg Leu Lys Ser
  59             85                  90                  95
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61 cca aac gaa ttt gct tca aat gct tta tac gaa aac aca ggt atg gta       336
62 Pro Asn Glu Phe Ala Ser Asn Ala Leu Tyr Glu Asn Thr Gly Met Val
63             100                 105                 110
65 agt gat ttt gtc act att atg aat cct aat gga gca tct tta aca atc       384
66 Ser Asp Phe Val Thr Ile Met Asn Pro Asn Gly Ala Ser Leu Thr Ile
67             115                 120                 125
69 tgg gct tta aat cct ggc aat tgg ata tgg gga tat agt tta ttt gct       432
70 Trp Ala Leu Asn Pro Gly Asn Trp Ile Trp Gly Tyr Ser Leu Phe Ala
71     130                 135                 140
73 agt aga cct ttt gga gat gca aga gct tgg cag ctt att gaa ttt cca       480
74 Ser Arg Pro Phe Gly Asp Ala Arg Ala Trp Gln Leu Ile Glu Phe Pro
75 145                 150                 155                 160
77 aac aat aca gta atg att aaa aat gca aaa aca ttt act tgc tta aac       528
78 Asn Asn Thr Val Met Ile Lys Asn Ala Lys Thr Phe Thr Cys Leu Asn
79             165                 170                 175
81 gcc tat aga aat ggc atc gtt cat tat cct tgt gat caa aca aat ttt       576
82 Ala Tyr Arg Asn Gly Ile Val His Tyr Pro Cys Asp Gln Thr Asn Phe
83             180                 185                 190
85 gcg cag ttt tgg aga ctt tat ccg atg act aat gga gct tat caa att       624
86 Ala Gln Phe Trp Arg Leu Tyr Pro Met Thr Asn Gly Ala Tyr Gln Ile
87             195                 200                 205
89 caa aat ttt gcc acc caa caa tgt ata caa aca cct gtt tca aat gta       672
90 Gln Asn Phe Ala Thr Gln Gln Cys Ile Gln Thr Pro Val Ser Asn Val
91 210                 215                 220
93 atg gaa gaa ttt aat ttg agc ttt tat aat att tat tta acc gat tgt       720
94 Met Glu Glu Phe Asn Leu Ser Phe Tyr Asn Ile Tyr Leu Thr Asp Cys
95 225                 230                 235                 240
97 ttg aaa gaa aaa gaa aag aat ttg gat aga cag tgg tat ata ggc gct       768
98 Leu Lys Glu Lys Glu Lys Asn Leu Asp Arg Gln Trp Tyr Ile Gly Ala
99             245                 250                 255
101 cct att taa ttttttcgct atgaaaggaa gata atg aaa aaa ata gta ttt       819
102 Pro Ile                                 Met Lys Lys Ile Val Phe
103                                             260
105 ttg att tta agt ttt aat gta tta ttt gcc gct tta gaa aat tac aac      867
106 Leu Ile Leu Ser Phe Asn Val Leu Phe Ala Ala Leu Glu Asn Tyr Asn
107 265                 270                 275                 280
109 acc gga act tgg aat ttg caa ggc tca tca gct gca act gaa agc aaa      915
110 Thr Gly Thr Trp Asn Leu Gln Gly Ser Ser Ala Ala Thr Glu Ser Lys
111                 285                 290                 295
113 tgg aat gtt agt ata aga caa ctc ata acc ggt gca aat cct atg gat      963
114 Trp Asn Val Ser Ile Arg Gln Leu Ile Thr Gly Ala Asn Pro Met Asp
115             300                 305                 310
117 gtt tta gct gtt caa gaa gcg ggg gtt tta cct agt aca gct atg atg     1011
118 Val Leu Ala Val Gln Glu Ala Gly Val Leu Pro Ser Thr Ala Met Met
119             315                 320                 325
121 act cct aga cag gta caa ccc gtg ggc gtg ggt att cct ata cat gaa     1059
122 Thr Pro Arg Gln Val Gln Pro Val Gly Val Gly Ile Pro Ile His Glu
123             330                 335                 340
125 tac ata tgg aat tta ggc tct gta tca aga cct agc tct gtt tat ata     1107
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126 Tyr Ile Trp Asn Leu Gly Ser Val Ser Arg Pro Ser Ser Val Tyr Ile
127 345                 350                 355                 360
129 tat tat tct aga gtg gat gta gga gca aat cgt gtg aat tta gct atc      1155
130 Tyr Tyr Ser Arg Val Asp Val Gly Ala Asn Arg Val Asn Leu Ala Ile
131                 365                 370                 375
133 gtt agc aga gtg caa gcg gat gaa gtt ttt gtt tta ccc cct cca aca      1203
134 Val Ser Arg Val Gln Ala Asp Glu Val Phe Val Leu Pro Pro Pro Thr
135                 380                 385                 390
137 gtt gct tca aga cct att ata ggc ata cgc ata ggc aat gat gct ttt      1251
138 Val Ala Ser Arg Pro Ile Ile Gly Ile Arg Ile Gly Asn Asp Ala Phe
139                 395                 400                 405
141 ttc aat ata cac gct cta gca agt ggg gga aat gac gca gga gcc att      1299
142 Phe Asn Ile His Ala Leu Ala Ser Gly Gly Asn Asp Ala Gly Ala Ile
143         410                 415                 420
145 gtc gct gct gtg gat atg ttt ttt aga aat aga cct gat att aat tgg      1347
146 Val Ala Ala Val Asp Met Phe Phe Arg Asn Arg Pro Asp Ile Asn Trp
147 425                 430                 435                 440
149 atg att tta ggc gat ttt aat aga gaa tca ggc gcc tta gta acc ttg      1395
150 Met Ile Leu Gly Asp Phe Asn Arg Glu Ser Gly Ala Leu Val Thr Leu
151                 445                 450                 455
153 cta gat cct gac tta aga gca cgc act cgc gta gtt gtt ccg cct tct      1443
154 Leu Asp Pro Asp Leu Arg Ala Arg Thr Arg Val Val Val Pro Pro Ser
155                 460                 465                 470
157 tct acg caa aca agt gga aga acg att gat tat gct atc act gga aat      1491
158 Ser Thr Gln Thr Ser Gly Arg Thr Ile Asp Tyr Ala Ile Thr Gly Asn
159                 475                 480                 485
161 tcc aac act gca gct tta tac aac cca cca ccg ata gtt gcg att tta      1539
162 Ser Asn Thr Ala Ala Leu Tyr Asn Pro Pro Pro Ile Val Ala Ile Leu
163         490                 495                 500
165 gct tta gaa gga tta aga acc ttt ttg gct tca gat cat ttt cct gta      1587
166 Ala Leu Glu Gly Leu Arg Thr Phe Leu Ala Ser Asp His Phe Pro Val
167 505                 510                 515                 520
169 aat ttt aga aga cct tag gagcttaat atg aaa aaa ttt ttt att tta ttt    1638
170 Asn Phe Arg Arg Pro             Met Lys Lys Phe Phe Ile Leu Phe
171                 525                             530
173 ttt gcc ctt ttg agc ttt ttg aaa gca gag cct agc ttg gat gaa tta      1686
174 Phe Ala Leu Leu Ser Phe Leu Lys Ala Glu Pro Ser Leu Asp Glu Leu
175         535                 540                 545
177 gca gac ttt act cct atg ttt gct ata aga tct tta gaa aca gga att      1734
178 Ala Asp Phe Thr Pro Met Phe Ala Ile Arg Ser Leu Glu Thr Gly Ile
179 550                 555                 560                 565
181 tct tta agt cct ttt aga aaa act tca aaa agg tta gaa gat caa aat      1782
182 Ser Leu Ser Pro Phe Arg Lys Thr Ser Lys Arg Leu Glu Asp Gln Asn
183                 570                 575                 580
185 tgg ttt tta aaa gag att gta gca aat gat gag cta aaa gct agg gat      1830
186 Trp Phe Leu Lys Glu Ile Val Ala Asn Asp Glu Leu Lys Ala Arg Asp
187                 585                 590                 595
189 atg cac gca aaa gat ttg cct ttt ggc tat gtt cag ttt ata agc cct      1878
190 Met His Ala Lys Asp Leu Pro Phe Gly Tyr Val Gln Phe Ile Ser Pro
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191         600               605               610
193 agg ggc gat gat ata tgc cta gct gtt tta agt gaa aaa agt ttt ggc    1926
194 Arg Gly Asp Asp Ile Cys Leu Ala Val Leu Ser Glu Lys Ser Phe Gly
195         615               620               625
197 acc aaa tct tgc aaa caa gat ttg caa gat gga aca atg cag act att    1974
198 Thr Lys Ser Cys Lys Gln Asp Leu Gln Asp Gly Thr Met Gln Thr Ile
199 630               635               640               645
201 ttt tct atc ata cca atg aca aat ggt tct ata caa att aga tct tta    2022
202 Phe Ser Ile Ile Pro Met Thr Asn Gly Ser Ile Gln Ile Arg Ser Leu
203               650               655               660
205 acc aat ggt ggc aat caa tgc atg agc act ttt cct gac tct agt atc    2070
206 Thr Asn Gly Gly Asn Gln Cys Met Ser Thr Phe Pro Asp Ser Ser Ile
207               665               670               675
209 gcc ata gaa aat cgc ttt ggt tta gga gaa tgc ctt ttg gat cgt tct    2118
210 Ala Ile Glu Asn Arg Phe Gly Leu Gly Glu Cys Leu Leu Asp Arg Ser
211         680               685               690
213 atc gta act gta tta agc aaa ctt ttc ttt ttc tcc cct gct ata atc    2166
214 Ile Val Thr Val Leu Ser Lys Leu Phe Phe Phe Ser Pro Ala Ile Ile
215   695               700               705
217 gaa gca agc gca att tac taa cacttttcta acaaaaccaa gctt             2211
218 Glu Ala Ser Ala Ile Tyr
219 710               715
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223 <211> LENGTH: 258
224 <212> TYPE: PRT
225 <213> ORGANISM: Campylobacter coli
227 <400> SEQUENCE: 2
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231 Phe Leu Ala Cys Ser Ser Lys Glu Gln Gln Ile Asn Pro Leu Gly Arg
232               20                  25                  30
234 Ser Tyr Gly Lys Phe Asn Asp Asn Asp Pro Leu Lys Leu Gly Ser Lys
235         35                  40                  45
237 Pro Thr Pro Pro Val Lys Gln Lys Thr Pro Ser Leu Val Glu Gly Lys
238         50                  55                  60
240 Lys Phe Pro Ala Ile Pro Leu Val Pro Pro Val Ile Thr Pro Asn Thr
241 65                  70                  75                  80
243 Phe Lys Gly Asp Asn Ala Val Lys Gly Pro Leu Pro Arg Leu Lys Ser
244               85                  90                  95
246 Pro Asn Glu Phe Ala Ser Asn Ala Leu Tyr Glu Asn Thr Gly Met Val
247               100                 105                 110
249 Ser Asp Phe Val Thr Ile Met Asn Pro Asn Gly Ala Ser Leu Thr Ile
250         115                 120                 125
252 Trp Ala Leu Asn Pro Gly Asn Trp Ile Trp Gly Tyr Ser Leu Phe Ala
253         130                 135                 140
255 Ser Arg Pro Phe Gly Asp Ala Arg Ala Trp Gln Leu Ile Glu Phe Pro
256 145               150                 155                 160
258 Asn Asn Thr Val Met Ile Lys Asn Ala Lys Thr Phe Thr Cys Leu Asn
259               165                 170                 175
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261 Ala Tyr Arg Asn Gly Ile Val His Tyr Pro Cys Asp Gln Thr Asn Phe
262             180                 .185             190
264 Ala Gln Phe Trp Arg Leu Tyr Pro Met Thr Asn Gly Ala Tyr Gln Ile
265         195                 200                 205
267 Gln Asn Phe Ala Thr Gln Gln Cys Ile Gln Thr Pro Val Ser Asn Val
268         210                 215                 220
270 Met Glu Glu Phe Asn Leu Ser Phe Tyr Asn Ile Tyr Leu Thr Asp Cys
271 225                 230                 235             240
273 Leu Lys Glu Lys Glu Lys Asn Leu Asp Arg Gln Trp Tyr Ile Gly Ala
274             245                 250                 255
276 Pro Ile
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281 <211> LENGTH: 267
282 <212> TYPE: PRT
283 <213> ORGANISM: Campylobacter coli
285 <400> SEQUENCE: 3
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290             20                 25                 30
292 Ala Ala Thr Glu Ser Lys Trp Asn Val Ser Ile Arg Gln Leu Ile Thr
293         35                 40                 45
295 Gly Ala Asn Pro Met Asp Val Leu Ala Val Gln Glu Ala Gly Val Leu
296         50                 55                 60
298 Pro Ser Thr Ala Met Met Thr Pro Arg Gln Val Gln Pro Val Gly Val
299 65                 70                 75                 80
301 Gly Ile Pro Ile His Glu Tyr Ile Trp Asn Leu Gly Ser Val Ser Arg
302             85                 90                 95
304 Pro Ser Ser Val Tyr Ile Tyr Tyr Ser Arg Val Asp Val Gly Ala Asn
305             100                 105                 110
307 Arg Val Asn Leu Ala Ile Val Ser Arg Val Gln Ala Asp Glu Val Phe
308             115                 .120                 125
310 Val Leu Pro Pro Pro Thr Val Ala Ser Arg Pro Ile Ile Gly Ile Arg
311         130                 135                 140
313 Ile Gly Asn Asp Ala Phe Phe Asn Ile His Ala Leu Ala Ser Gly Gly
314 145                 150                 155                 160
316 Asn Asp Ala Gly Ala Ile Val Ala Ala Val Asp Met Phe Phe Arg Asn
317             165                 170                 175
319 Arg Pro Asp Ile Asn Trp Met Ile Leu Gly Asp Phe Asn Arg Glu Ser
320             180                 185                 190
322 Gly Ala Leu Val Thr Leu Leu Asp Pro Asp Leu Arg Ala Arg Thr Arg
323         195                 200                 205
325 Val Val Val Pro Pro Ser Ser Thr Gln Thr Ser Gly Arg Thr Ile Asp
326         210                 215                 220
328 Tyr Ala Ile Thr Gly Asn Ser Asn Thr Ala Ala Leu Tyr Asn Pro Pro
329 225                 230                 235                 240
331 Pro Ile Val Ala Ile Leu Ala Leu Glu Gly Leu Arg Thr Phe Leu Ala
332             245                 250                 255
334 Ser Asp His Phe Pro Val Asn Phe Arg Arg Pro
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/14/2006
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 3,6,12,18
Seq#:6; N Pos. 1,4,7,10,13,16,19
Seq#:7; N Pos. 6
Seq#:8; N Pos. 1,2,11,16
Seq#:10; N Pos. 13
Seq#:55; N Pos. 21,22,23,24,25,26,27,28,29
Seq#:58; N Pos. 21,22,23,24,25,26,27,28,29
Seq#:61; N Pos. 21,22,23,24,25,26,27,28,29

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30
Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,55,56,57,58
Seq#:59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79

VERIFICATION SUMMARY   DATE: 06/14/2006
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:1441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:1483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
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